SEQUENCE LISTING

<110> Ford, John
       Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
       POLYPEPTIDES

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<150> PCT/US99/16180
<151> 1999-07-16

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<151> 1999-07-09

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<170> PatentIn Ver. 2.0

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agcacttata agctctatac acatagttac ctgggatttg gattgaaagc tgcaagacta 240

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aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180

gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc cacccagcca catcttggga 240

aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290
      Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser
      1   5   10   15

tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag 338
Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
                20   25   30

ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc 386
Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
            35   40   45

ttg tat gga att atg ttt gat gca ggg agc act gga act cga att cat 434
Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His
        50   55   60

gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu
    65   70   75

ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat 530
Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp
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caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578
Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala
                100   105   110

aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta 626
Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu
            115   120   125

aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct 674
Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala
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ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta 722
Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val
        145   150   155

cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta 770
Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu
160   165   170   175

gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga 818
Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg
            180   185   190

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cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc    866
Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile
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acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc    914
Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly
            210                 215                 220

tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca    962
Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr
            225                 230                 235

cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg   1010
His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu
240                 245                 250                 255

gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc   1058
Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala
            260                 265                 270

tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa   1106
Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys
            275                 280                 285

tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc   1154
Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys
            290                 295                 300

tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag   1202
Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu
305                 310                 315

gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga   1250
Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg
320                 325                 330                 335

gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa   1298
Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys
            340                 345                 350

gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa   1346
Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu
            355                 360                 365

aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc   1394
Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile
            370                 375                 380

aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta   1442
Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu
385                 390                 395

cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg   1490
Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly
400                 405                 410                 415

gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tgaggccacg   1539
Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
            420                 425

tacttccttg gagacctgca tttgccaaca cctttttaag gggaggagag agcacttagt 1599
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ttctgaacta gtctggggac atcctggact tgagcctaga gattwrgtta attaascggc 1659

cgagcttatc cttwatragg taatttactt gcmtggccgc gtttacacgt cgtgatggna 1719

aacctgcgtc ccaactaacg cttgasamat ccccttcgca gctgcgatac caaaagccga 1779

cgacgccttc cacagtgcca   1799

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            20   25   30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
        35   40   45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
    50   55   60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65   70   75   80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
                85   90   95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
            100   105   110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
        115   120   125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
    130   135   140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145   150   155   160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
            165   170   175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
            180   185   190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
        195   200   205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
    210   215   220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225   230   235   240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly

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            245                  250                   255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
            260             265             270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
        275             280             285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
    290             295             300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
            340             345             350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
            355             360             365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
    370             375             380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395             400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
            405             410             415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt    96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
            20              25                  30

atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg   144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
        35              40                  45

tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt   192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
    50              55                  60
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tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg    240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65                  70                  75                  80

gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa    288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
                85                  90                  95

cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa    336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
               100                 105                 110

gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag    384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
               115                 120                 125

gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg    432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
           130                 135                 140

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca    480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145                 150                 155                 160

aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta gct    528
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
                165                 170                 175

tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag    576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
                180                 185                 190

gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg    624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
                195                 200                 205

ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac    672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
           210                 215                 220

ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca cat    720
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225                 230                 235                 240

agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga    768
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
                245                 250                 255

gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc tgt    816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
               260                 265                 270

tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac    864
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
           275                 280                 285

cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat    912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
           290                 295                 300
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gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag    960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320

gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct   1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335

gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt   1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
            340             345             350

gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac   1104
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
            355             360             365

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Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
    370             375             380

gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta cag   1200
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395             400

ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg gcc   1248
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
            405             410             415

acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tga               1287
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
            420             425
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            20                  25                  30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
            35                  40                  45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
        50                  55                  60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65                  70                  75                  80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
                85                  90                  95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
            100                 105                 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
            115                 120                 125
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Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
    130             135             140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145             150             155             160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
            165             170             175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
            180             185 .           190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
        195             200             205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
    210             215             220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225             230             235             240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
            245             250             255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
            260             265             270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
        275             280             285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
    290             295             300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
            340             345             350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
        355             360             365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
    370             375             380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395             400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
            405             410             415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
            420             425
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1               5                   10                  15

gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt    96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
                20                  25                  30

atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg   144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
            35                  40                  45

tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt   192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
        50                  55                  60

tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg   240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65                  70                  75                  80

gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa   288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
                85                  90                  95

cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa   336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
                100                 105                 110

gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag   384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
            115                 120                 125

gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg   432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
        130                 135                 140

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca   480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145                 150                 155                 160

aag ggc agt gtt agc atc atg act gga caa gac gaa ggc ata ttc gct   528
Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala
                165                 170                 175

tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag   576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
                180                 185                 190

gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg   624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
            195                 200                 205

ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac   672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
        210                 215                 220

ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca cat   720
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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225             230             235                 240

agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga    768
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
            245             250             255

gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc tgt    816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
            260             265             270

tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac    864
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
            275             280             285

cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat    912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
            290             295             300

gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag    960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320

gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct   1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335

gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt   1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
            340             345             350

gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac   1104
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
            355             360             365

ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca   1152
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
            370             375             380

gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta cag   1200
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395             400

ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg gcc   1248
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
            405             410             415

acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tga               1287
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
            420             425
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<210> 7
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<212> PRT
<213> Homo sapiens

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1               5               10                  15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
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                 20                      25                      30
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
        35              40              45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
    50              55              60          .
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65              70              75              80
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
            85              90              95
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
            100             105             110
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
        115             120             125
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
    130             135             140
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145             150             155             160
Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala
            165             170             175
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
        180             185             190  .
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
        195             200             205
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
    210             215             220
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225             230             235             240
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
            245             250             255
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
            260             265             270
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
        275             280             285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
    290             295             300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
        340             345             350
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Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
        355             360             365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
    370             375             380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395                 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
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Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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            Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val
             1   5   10

gta tcc tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg 158
Val Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp
    15   20   25

ttt gag ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc 206
Phe Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala
 30   35   40   45

agc acc ttg tat gga att atg ttt gat gca ggg agc act gga act cga 254
Ser Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg
             50   55   60

att cat gtt tac acc ttt gtg cag aaa atg cca g gtaagtgca actgggrccc 307
Ile His Val Tyr Thr Phe Val Gln Lys Met Pro
             65   70

ttagtagagt ctgtaaatcc acactttagc atctcctccc agaaacaaat atgctgagag 367

tttattatgt gaattacaga atctcacacc tagtggatgt ctttcttcag agaactttgg 427

actacaattg aacatgtggg ttatttattt attttattt atttgttttg tttttatttt 487

ttaacttttt ttttgagaca aggtcttgct ttgttgcccg tctgtagtg cagtggcatg 547

atgacacatc actgcaacct tgacctcctg ggctcaagca gtccttccac ctcagccccc 607

tgagttgttg agactacagg cttgtgccac catgcccagc tcatttttaa attttttttat 667

agagacctgc tcagactggc ctcaaactcc taggctcaat tgatcctccc acctcagcct 727

cccaaagtac tggattata ggtgtaagtc accatgcttg gccagaacac atggcttaat 787

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gagcccagca tctgaagcag cctaactttt ggtaaccagc tctctcttct gttttgttcc 1267

atgracaaaa tag ga cag ctt cca att cta gaa ggg gaa gtt ttt gat tct 1318
             Gly Gln Leu Pro Ile Leu Glu Gly Glu Val Phe Asp Ser
                  75   80   85

gtg aag cca gga ctt tct gct ttt gta gat caa cct aag cag ggt gct   1366
Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala
             90   95   100

gag acc gtt caa ggg ctc tta gag gtg gcc aaa gac tca atc ccc cga   1414
Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg
         105   110   115

agt cac tgg aaa aag acc cca gtg gtc cta aag gca aca gca gga cta   1462
Ser His Trp Lys Lys Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu
         120   125   130

cgc tta ctg cca gaa cac aaa gcc aag gct ctg ctc ttt gag gta aag   1510
Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu Leu Phe Glu Val Lys
    135   140   145

gag atc ttc agg aag tca cct ttc ctg gta cca aag ggc agt gtt agc   1558
Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro Lys Gly Ser Val Ser
150   155   160   165

atc atg gat gga tcc gac gaa g gtgggagag gtgttgatat gcgttccagg   1609
Ile Met Asp Gly Ser Asp Glu
                170

gggagagggg caggatcagt gaaagatcta actaaaggaa ctggggccag gaataaacag 1669

aaggaatgag atagcaggaa atagaagaca gggagaaggg aacatgtgct ctagacatgg 1729

aatttagaga ggaaaaaaaa aaaacaaggt tggggccagg aaagagaaaa aatgctctgg 1789

gatctaatcc ttgtctttct ttctttttag gc ata tta gct tgg gtt act gtg 1842
                                  Gly Ile Leu Ala Trp Val Thr Val
                                       175   180

aat ttt ctg aca g gtaatacat cctcaagttt atctttagag cttaactagc   1894
Asn Phe Leu Thr

ttttacatgc atagtcagag gagtaaaagc ctcttctttc attctgtatt gtttcttctt 1954

ctttaaaaaa ggaaaagagg ctgggtgtgg cagttcatgc ctgttaattc cagcgctttg 2014

ggaggctgag ttgggcagat cacttgaggc caggagttca agaccagcct ggccaacatg 2074

gcgaaactcc gtctctacca aaaatacaaa aatagctggg catggtggtg tgtacctgta 2134

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ggaatacctt cagtgtatga taagagcaag agagacaagt gttgggctgc·ccaggatgtc 2434

gaggctattt agagctggct ctcatttgac ag gt cag ctg cat ggc cac aga   2486
                                    Gly Gln Leu His Gly His Arg
                                    185   190   ·

cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc   2534
Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile
        195   200   205

acg ttc ctg ccc cag ttt gag gtgagtcatt taatgaagat ctggttagaa   2585
Thr Phe Leu Pro Gln Phe Glu
        210

gtgcacttgg caggcgtatc atggtgccaa gaaagaggcg ccccatttc agccagcagc 2645

tctaccacgc ttaggcagag tcaagtcaat taataactag gtgaatgttc ccttgccatc 2705

tcactgttca gaatcccttc gtttcctcaa gcctagtgag attagcccct taatctgtct 2765

tcatctctga ttttttgctg ggagggacgg gtggtggtgt gaacatcttc aggtaattac 2825

agatcctgaa tagctttttg ctttttctga tttgcag aaa act ctg gaa caa amt 2880
                                            Lys Thr Leu Glu Gln Xaa
                                            215   220

cya trg ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag   2928
Xaa Xaa Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys
            225   230   235

ctc tat aca cat ag gtgaggac ggggacaggg aagaagaata tttmwtkttg   2980
Leu Tyr Thr His
            240

tatgatksty ytamctktss maagcwtkct caaatctstk aytkyatctg attmgcaaaa 3040

acaaagdctg tgccaattcc ctaaggccta tcaactgaaa cccggwccac ttacaaagcc 3100

ggaggagcct aagaggcttc tccattcttg gcctcaaaag cattaatata tgacttaaga 3160

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gaggtgggtg ggtcacctga ggtcaggcgt ttragaccag cctggcaaac atggtgaaac 3280

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gaaagaggta gctttaggct agagaacttc aggaccagca tgaaattagt caatcctgta 3880

ttttacag t tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc 3928
          Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr
              245   250

ctg gga gcc ctg gag aca gaa g gtttgtctggt acctgtgctg gggggggatg 3982
Leu Gly Ala Leu Glu Thr Glu Gly
255   260

gtgagggtga cacagatact ccgcttgctt cttcccttcc ttgatagcca ttctatggag 4042

gaaaagatta tgttgaattg ggaggcaaat gttgtataat ggacctaata atggcaaact 4102

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tggaattaat ttcataggat tttaaggccc agcccccatg gtgaytcttt tccacctcac 4822

tggcttcttg cttgccttcc tccctctctc tcacttactt acctcttacc ttgtgccctg 4882

gattctttcag gg act gat ggg cac act ttc cgg agt gcc tgt tta ccg   4931
            Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu Pro
                265   270

aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac cag tat 4979
Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln Tyr
275   280   285   290

ggt ggc aac caa gaa g gcaagtgat gttttttcac tggttaaagt tacgtttaca 5034
Gly Gly Asn Gln Glu
            295

atggaagctc tggaaaagtc ccatgggaaa ctttttccag aactcaagag aagcttatct 5094

tgttgcaggg asttattcca aagatcttgg catgcctcca aggactaatg tgaagtgaca 5154

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tcaccttacc cctgtgcacc tttgcctggc ag gg gag gtg ggc ttt gag ccc   5866
                                  Gly Glu Val Gly Phe Glu Pro
                                               300

tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca   5914
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro
           305   310   315

gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac   5962
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp
           320   325   330

cga gct gtt gac aca gac atg att g gtgagttca ccccaggtgt cagtccagag 6016
Arg Ala Val Asp Thr Asp Met Ile
335   340

aggaaggtgg atagggctgt ggtggggaag gtcaaggaga aagagcactt gaggtgcttt 6076

gtcggggtga ttacccacct cttttctagt cactcgaaca aaagggtgga aatgacttag 6136

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gttgcataga ttacattatg tacatgtgta tataatgaat gaatgaatga ·atttccttat 6916

gcttccttga aggcgttttg atatcagata atcttctgtt ttatttcag at tat gaa   6973
                                                          Asp Tyr Glu
                                                              345

aag ggg ggt att tta aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa   7021
Lys Gly Gly Ile Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu
            350   355   360

gtg tgt gat aac ttg gaa aac ttc acc tca ggc agt cct ttc ctg tgc   7069
Val Cys Asp Asn Leu Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys
            365   370   375

atg gat ctc agc tac atc aca gcc ctg tta aag gat ggc ttt ggc ttt   7117
Met Asp Leu Ser Tyr Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe
            380   385   390

gca gac agc aca gtc tta cag gtaagagaca ggacaccaga gtctcataac   7168
Ala Asp Ser Thr Val Leu Gln
            395   400

agccctcttt tgtgggggtt gagaaggagt aagagcttgt tcagtaatca gagtagctag 7228

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gaatgtggga aattatctca atgcaatggt agcctccgag tgtattacca ggcaagctat 7348

cgcacaggtc acagaacaga aagactagca gcccaaatta agatgccaag tcacatggtt 7408

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ccctagatct attctcacct cctgaccatg ctctttctgc cacatctatt atcattacaa 8188

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aacgttaggg aaagttcaga atactgtctg tctaaactat ctctctagaa ggcctgatgg 8308

gccacaacct gggccagaag cattcagttc agatatgaga atggtgggtg taggggcaat 8368

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ccaagagctg tgcttgctag agttggaaac tggatgaaaa ggtgaagact ttttttct.:c 8548
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```
tcaacag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg       8597
        Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
                        405                     410
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```
ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat             8639
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
415                 420                 425
```

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agcacttagt ttctgaacta gtctggggac atcctggact tgagcctaga gatttaggtt 8759

taattaattt tacacatcta atagtgaact gctgcctaac cactcaagag tacacagctg 8819

gcaccagagc atcacagaga gccctgtgag ccaaaaagta tagttttgga acttaacctt 8879

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gagtgcctca ttccactgaa tatttaaatt ttcctcttaa atgggaaact gacttattgc 8999

aatcccaaga cccatcaata tcagtatttt tttcctccct atacaggggcc ctgcccaccc 9059

ttatctgcac ccacctcccc tgaaaaagag agaaaaaaaa aaamccbggt tttgctttcc 9119

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 10
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<212> DNA
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
ctggctggtg aagttttcct c   21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
gcaggtctcc aaggaagtac g   21

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
gtgagtgctc cctgcatcta acataattcc   30

<210> 13
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 14
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
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<210> 15
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<220>
<223> Description of Artificial Sequence: primer

<400> 15
gcaacagcag gactacgctt actgccagaa c   31

<210> 16
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
cccaagcgaa tatgccttcg tcttgtccag tcatgatgct aacactgc   48

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
cgaaggcata ttcgcttggg ttactgtg   28

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
cttccttcac tgggaattca gg   22

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
ctgtttaccg agatggttgg aagc   24

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20
ttaaagcttg ggaaaagaat ggccacttc   29

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agactcgagg tggctcaatg ggagatgcc   29

<210> 22
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
gcgctgtctc ccacagagga tcgcatcacc atcaccatca caaccagcag acttggtt   58

<210> 23
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
aaccaagtct gctggttgtg atggtgatgg tgatgcgatc ctctgtggga gacagcgc   58

<160> 2

<170> PatentIn Ver. 2.0

<210> 24
<211> 1601
<212> DNA
<213> Homo sapiens

<400> 24
gcgggctgcc gcgcaagggt ggcgcgcgcg cgttttcctt gttcctggtc aacaaagaaa 60
tgtggagtgt cttggctgaa tcctcataca gacaagatca ttatggtgct gttaggttga 120
aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180
gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc cacccagcca catcttggga 240
aaagaatggc cacttcttgg ggcacagtct ttttcatgct ggtggtatcc tgtgtttgca 300
gcgctgtctc ccacaggaac cagcagactt ggtttgaggg tatcttcctg tcttccatgt 360
gccccatcaa tgtcagcgcc agcaccttgt atggaattat gtttgatgca gggagcactg 420
gaactcgaat tcatgtttac acctttgtgc agaaaatgcc aggacagctt ccaattctag 480
aaggggaagt ttttgattct gtgaagccag actttctgc ttttgtagat caacctaagc 540
agggtgctga accgttcaa gggctcttag aggtggccaa agactcaatc ccccgaagtc 600
actggaaaaa gaccccagtg gtcctaaagg caacagcagg actacgctta ctgccagaac 660
acaaagccaa ggctctgctc tttgaggtaa aggagatctt caggaagtca cctttcctgg 720
taccaaaggg cagtgttagc atcatggatg gatccgacga aggcatatta gcttgggtta 780

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ctgtgaattt tctgacaggt cagctgcatg gccacagaca ggagactgtg gggaccttgg 840
acctaggggg agcctccacc caaatcacgt tcctgcccca gtttgagaaa actctggaac 900
aaactcctag gggctacctc acttcctttg agatgtttaa cagcacttat aagctctata 960
cacatagtta cctgggattt ggattgaaag ctgcaagact agcaaccctg ggagccctgg 1020
agacagaagg gactgatggg cacactttcc ggagtgcctg tttaccgaga tggttggaag 1080
cagagtggat ctttgggggt gtgaaatacc agtatggtgg caaccaagaa ggggaggtgg 1140
gctttgagcc ctgctatgcc gaagtgctga gggtggtacg aggaaaactt caccagccag 1200
aggaggtcca gagaggttcc ttctatgctt tctcttacta ttatgaccga gctgttgaca 1260
cagacatgat tgattatgaa aagggggggta ttttaaaagt tgaagatttt gaaagaaaag 1320
ccagggaagt gtgtgataac ttggaaaact tcacctcagg cagtcctttc ctgtgcatgg 1380
atctcagcta catcacagcc ctgttaaagg atggctttgg ctttgcagac agcacagtct 1440
tacaggctgc cgtactgagg tgatgggcca agctggagat atccccaaag cccatgttga 1500
caccctgtcc tgcaagcgga tggactctgt gggctgcatc cctaagaata aagcagagtt 1560
caggtgtgac ctctggcagc aaaaaaaaaa aaaaaaaaa a 1601
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<210> 25
<211> 405
<212> PRT
<213> Homo sapiens

<400> 25

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Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1               5                  10                  15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
                 20                  25                  30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
             35                  40                  45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
         50                  55                  60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65                  70                  75                  80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
                 85                  90                  95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
                100                 105                 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
             115                 120                 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
         130                 135                 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145                 150                 155                 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
                 165                 170                 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
                 180                 185                 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
             195                 200                 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
         210                 215                 220
```

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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225             230             235             240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
            245             250             255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
            260             265             270


Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
        275             280             285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
    290             295             300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305             310             315             320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
            325             330             335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
            340             345             350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
        355             360             365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
    370             375             380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385             390             395             400

Ala Ala Val Leu Arg
                405

<210> 26
<211> 2762
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (148)..(1599)

<400> 26
gtggggtcgt atcccgcggg tggaggccgg ggtggcgccg gccggggcgg gggagcccaa 60

aagaccggct gccgcctgct ccccggaaaa gggcactcgt ctccgtgggt gtggcggagc 120

gcgcggtgca tggaatgggc tatgtga atg aaa aaa ggt atc cgt tat gaa act 174
                               Met Lys Lys Gly Ile Arg Tyr Glu Thr
                                1               5

tcc aga aaa acg agc tac att ttt cag cag ccg cag cac ggt cct tgg 222
Ser Arg Lys Thr Ser Tyr Ile Phe Gln Gln Pro Gln His Gly Pro Trp
 10              15              20              25

caa aca agg atg aga aaa ata tcc aac cac ggg agc ctg cgg gtg gcg 270
Gln Thr Arg Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala
            30              35              40
```

```
aag gtg gca tac ccc ctg ggg ctg tgt gty ggc gtg ttc atc tat gtt    318
Lys Val Ala Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val
             45                  50                  55

gcc tac atc aag tgg cac cgg gcc acc gcc acc cag gcc ttc ttc agc    366
Ala Tyr Ile Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser
             60                  65                  70

atc acc agg gca gcc ccg ggg gcc cgg tgg ggt cag cag gcc cac agc    414
Ile Thr Arg Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser
         75                  80                  85

ccc ctg ggg aca gct gca gac ggg cac gag gtc ttc tac ggg atc atg    462
Pro Leu Gly Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met
     90                  95                 100                 105

ttt gat gca gga agc act ggc acc cga gta cac gtc ttc cag ttc acc    510
Phe Asp Ala Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr
                     110                 115                 120

cgg ccc ccc aga gaa act ccc acg tta acc cac gaa acc ttc aaa gca    558
Arg Pro Pro Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala
             125                 130                 135

gtg aag cca ggt ctt tct gcc tat gct gat gat gtt gaa aag agc gct    606
Val Lys Pro Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala
             140                 145                 150

cag gga atc cgg gaa cta ctg gat gtt gct aaa cag gac att ccg ttc    654
Gln Gly Ile Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe
         155                 160                 165

gac ttc tgg aag gcc acc cct ctg gtc ctc aag gcc aca gct ggc tta    702
Asp Phe Trp Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu
170                 175                 180                 185

cgc ctg tta cct gga gaa aag gcc cag aag tta ctg cag aag gtg aaa    750
Arg Leu Leu Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys
                 190                 195                 200

gaa gta ttt aaa gca tcg cct ttc ctt gta ggg gat gac tgt gtt tcc    798
Glu Val Phe Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser
             205                 210                 215

atc atg aac gga aca gat gaa ggc gtt tcg gcg tgg atc acc atc aac    846
Ile Met Asn Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn
             220                 225                 230

ttc ctg aca ggc agc ttg aaa act cca gga ggg agc agc gtg ggc atg    894
Phe Leu Thr Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met
         235                 240                 245

ctg gac ttg ggc gga gga tcc act cag atc gcc ttc ctg cca cgc gtg    942
Leu Asp Leu Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val
250                 255                 260                 265

gag ggc acc ctg cag gcc tcc cca ccc ggc tac ctg acg gca ctg cgg    990
Glu Gly Thr Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg
                 270                 275                 280
```

```
atg ttt aac agg acc tac aag ctc tat tcc tac agc tac ctc ggg ctc   1038
Met Phe Asn Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu
            285             290             295

ggg ctg atg tcg gca cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag   1086
Gly Leu Met Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln
            300             305             310

cct gct aag gat gga aag gag ttg gtc agc cct tgc ttg tct ccc agt   1134
Pro Ala Lys Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser
            315             320             325

ttc aaa gga gag tgg gaa cac gca gaa gtc acg tac agg gtt tca ggg   1182
Phe Lys Gly Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly
330             335             340             345

cag aaa gca gcg gca agc ctg cac gag ctg tgt gct gcc aga gtg tca   1230
Gln Lys Ala Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser
            350             355             360

gag gtc ctt caa aac aga gtg cac agg acg gag gaa gtg aag cat gtg   1278
Glu Val Leu Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val
            365             370             375

gac ttc tat gct ttc tcc tac tat tac gac ctt gca gct ggt gtg ggc   1326
Asp Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly
            380             385             390

ctc ata gat gcg gag aag gga ggc agc ctg gtg gtg ggg gac ttc gag   1374
Leu Ile Asp Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu
            395             400             405

atc gca gcc aag tac gtg tgt cgg acc ctg gag aca cag ccg cag agc   1422
Ile Ala Ala Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser
410             415             420             425

agc ccc ttc tca tgc atg gac ctc acc tac gtc agc ctg cta ctc cag   1470
Ser Pro Phe Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln
            430             435             440

gag ttc ggc ttt ccc agg agc aaa gtg ctg aag ctc act cgg aaa att   1518
Glu Phe Gly Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile
            445             450             455

gac aat gtt gag acc agc tgg gct ctg ggg gcc att ttt cat tac atc   1566
Asp Asn Val Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile
            460             465             470

gac tcc ctg aac aga cag aag agt cca gcc tca tagtggccga gccatccctg 1619
Asp Ser Leu Asn Arg Gln Lys Ser Pro Ala Ser
475             480

tccccgtcag cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcatc 1679

ctgaggagcc acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca 1739

gaaggcctgg tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc 1799

tggacctggg ccctgctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg 1859

acagaaccac aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg 1919
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cccgtccgc gggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc 1979

cagcctgtca gtttcctccc cagggcagag ctcccttcc tgcaagagtc tgggaggcgg 2039

tgcaggctgt cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag 2099

taggtctggg cggcaccact gggaactctg gacttgagtg tgtttgctct tccttgggta 2159

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tgatggaggg agacacctct tcatagacgg caggtgccca cctttcaggg agtctcccag 2279

catgggcgga tgccgggcat gagctgctgt aaactatttg tggctgtgct gcttgagtga 2339

cgtctctgtc gtgtgggtgc caagtgcttg tgtagaaact gtgttctgag cccccttttc 2399

tggacaccaa ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg 2459

gccatgtctt aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct 2519

ctcggtgtct cgggccacca tccgcccacc tcgggctgac cccacctcct ccatggacag 2579

tgtgagcccc gggccgtgca tcctgctcag tgtggcgtca gtgtcggggc tgagcccctt 2639

gagctgcttc agtgaatgta cagtgcccgg cacgagctga acctcatgtg ttccactccc 2699

aataaaaggt tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2759

aaa                                                              2762
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<210> 27
<211> 484
<212> PRT
<213> Homo sapiens

<400> 27
Met Lys Lys Gly Ile Arg Tyr Glu Thr Ser Arg Lys Thr Ser Tyr Ile
1               5                   10                  15

Phe Gln Gln Pro Gln His Gly Pro Trp Gln Thr Arg Met Arg Lys Ile
                20                  25                  30

Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro Leu Gly
            35                  40                  45

Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp His Arg
        50                  55                  60

Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala Pro Gly
65                  70                  75                  80

Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala Ala Asp
                85                  90                  95

Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly
            100                 105                 110

Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu Thr Pro
        115                 120                 125

Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu Ser Ala
```

```
           130                    135                    140
Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu Leu Leu
145             150             155             160

Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala Thr Pro
                165             170              175

Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly Glu Lys
            180             185             190

Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala Ser Pro
            195             200             205

Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr Asp Glu
    210             215             220

Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser Leu Lys
225             230             235             240

Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly Gly Ser
            245             250             255

Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln Ala Ser
            260             265             270

Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr Tyr Lys
        275             280             285

Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala Arg Leu
    290             295             300

Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly Lys Glu
305             310             315             320

Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp Glu His
            325             330             335


Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala Ser Leu
        340             345             350

His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn Arg Val
        355             360             365

His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe Ser Tyr
    370             375             380

Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu Lys Gly
385             390             395             400

Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr Val Cys
            405             410             415

Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys Met Asp
        420             425             430

Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro Arg Ser
        435             440             445

Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr Ser Trp
450             455             460
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Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg Gln Lys
465             470             475             480

Ser Pro Ala Ser
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<210> 28
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
cgtatcccgc gggtggaggc cggggtg   27

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
cttctgcaag tcccagagcc agtgtgc   27

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
ggagcccaaa agaccggctg c   21

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
tgaagtcacg tccaggacag g   21

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
cggaattcaa catgaaaaaa ggtaatccgt tatgaa   36

<210> 33
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:.primer

<400> 33
tgtctagatg aggctggact cttctg   26

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide primer

<400> 34
atcctggact tgagcctaga g   21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide primer

<400> 35
ctgatattga tgggtcttgg g   21

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide primer

<400> 36
ggatggaaag gagttggtca g   21

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

oligonucleotide primer

<400> 37
gtccacatgc ttcacttcct c   21